

Figure 1

	ATG TCA AAT ATT ACA GAT CCA CAG ATG TGG GAT TTT 86
	Met Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe
	1 5 10
5	GAT GAT CTA AAT TTC ACT GGC ATG CCA CCT GCA GAT GAA 125
	Asp Asp Leu Asn Ph Thr Gly Met Pro Pro Ala Asp Glu
	15 20 25
10	GAT TAC AGC CCC TGT ATG CTA GAA ACT GAG ACA CTC AAC 164
	Asp Tyr Ser Pro Cys Met Leu Glu Thr Glu Thr Leu Asn
	30 35
15	AAG TAT GTT GTG ATC ATC GCC TAT GCC CTA GTG TTC CTG 203
	Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu Val Phe Leu
	40 45 50
20	CTG AGC CTG CTG GGA AAC TCC CTG GTG ATG CTG GTC ATC 242
	Leu Ser Leu Leu Gly Asn Ser Leu Val Met Leu Val Ile
	55 60
25	TTA TAC AGC AGG GTC GGC CGC TCC GTC ACT GAT GTC TAC 281
	Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr
	65 70 75
30	CTG CTG AAC CTG GCC TTG GCC GAC CTA CTC TTT GCC CTG 320
	Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu
	80 85 90
35	ACC TTG CCC ATC TGG GCC GCC TCC AAG GTG AAT GGC TGG 359
	Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp
	95 100
40	ATT TTT GGC ACA TTC CTG TGC AAG GTG GTC TCA CTC CTG 398
	Ile Phe Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu
	105 110 115
45	AAG GAA GTC AAC TTC TAC AGT GGC ATC CTG CTG TTG GCC 437
	Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu Leu Leu Ala
	120 125
50	TGC ATC AGT GTG GAC CGT TAC CTG GCC ATT GTC CAT GCC 476
	Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His Ala
	130 135 140
55	ACA CGC ACA CTG ACC CAG AAG CGT CAC TTG GTC AAG TTT 515
	Thr Arg Thr Leu Thr Gln Lys Arg His Leu Val Lys Phe
	145 150 155
60	GTT TGT CTT GGC TGC TGG GGA CTG TCT ATG AAT CTG TCC 554
	Val Cys Leu Gly Cys Trp Gly Leu Ser Met Asn Leu Ser
	160 165
65	CTG CCC TTC TTC CTT TTC CGC CAG GCT TAC CAT CCA AAC 593
	Leu Pro Phe Phe Leu Phe Arg Gln Ala Tyr His Pro Asn
	170 175 180
70	AAT TCC AGT CCA GTT TGC TAT GAG GTC CTG GGA AAT GAC 632

Fig. 2a

	Asn Ser Ser Pro Val Cys Tyr Glu Val Leu Gly Asn Asp	
	185	190
5	ACA GCA AAA TGG CGG ATG GTG TTG CGG ATC CTG CCT CAC 671	
	Thr Ala Lys Trp Arg M t Val Leu Arg Ile Leu Pro His	
	195	200 205
10	ACC TTT GGC TTC ATC GTG CCG CTG TTT GTC ATG CTG TTC 710	
	Thr Phe Gly Phe Ile Val Pro Leu Phe Val Met Leu Phe	
	210	215 220
15	TGC TAT GGA TTC ACC CTG CGT ACA CTG TTT AAG GCC CAC 749	
	Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His	
	225	230
20	ATG GGG CAG AAG CAC CGA GCC ATG AGG GTC ATC TTT GCT 788	
	Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala	
	235	240 245
25	GTC GTC CTC ATC TTC CTG CTT TGC TGG CTG CCC TAC AAC 827	
	Val Val Leu Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn	
	250	255
30	CTG GTC CTG CTG GCA GAC ACC CTC ATG AGG ACC CAG GTG 866	
	Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr Gln Val	
	260	265 270
35	ATC CAG GAG ACC TGT GAG CGC CGC AAC AAC ATC GGC CGG 905	
	Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg	
	275	280 285
40	GCC CTG GAT GCC ACT GAG ATT CTG GGA TTT CTC CAT AGC 944	
	Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu His Ser	
	290	295
45	TGC CTC AAC CCC ATC ATC TAC GCC TTC ATC GGC CAA AAT 983	
	Cys Leu Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn	
	300	305 310
50	TTT CGC CAT GGA TTC CTC AAG ATC CTG GCT ATG CAT GGC 1022	
	Phe Arg His Gly Phe Leu Lys Ile Leu Ala Met His Gly	
	315	320
55	CTG GTC AGC AAG GAG TTC TTG GCA CGT CAT CGT GTT ACC 1061	
	Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val Thr	
	325	330 335
60	TCC TAC ACT TCT TCG TCT GTC AAT GTC TCT TCC AAC CTC 1100	
	Ser Tyr Thr Ser Ser Ser Val Asn Val Ser Ser Asn Leu	
	340	345 350
65	TGAAAACCAT CGATGAAGGA ATATCTCTTC TCAGAAGGAA AGAATAACCA 1150	
70	ACACCCTGAG GTTGTGTGTG GAAGGTGATC TGGCTCTGGA CAGGCACTAT 1200	
75	CTGGGTTTTG GGGGGACGCT ATAGGATGTG GGGAAAGTTAG GAACTGGTGT 1250	

Fig. 2b

CTTCAGGGGC CACACCAACC TTCTGAGGAG CTGTTGAGGT ACCTCCAAGG 1300
5 ACCGGCCTTT GCACCTCCAT GGAAACGAAG CACCATCATT CCCGTTGAAC 1350
GTCACATCTT TAACCCACTA ACTGGCTAAT TAGCATGGCC ACATCTGAGC 1400
10 CCCGAATCTG ACATTAGATG AGAGAACAGG GCTGAAGCTG TGTCTCATG 1450
AGGGCTGGAT GCTCTCGTTG ACCCTCACAG GAGCATCTCC TCAACTCTGA 1500
GTGTTAAGCG TTGAGCCACC AAGCTGGTGG CTCTGTGTGC TCTGATCCGA 1550
20 GCTCAGGGGG GTGGTTTTCC CATCTCAGGT GTGTTGCAGT GTCTGCTGGA 1600
GACATTGAGG CAGGCACTGC CAAAACATCA ACCTGCCAGC TGGCCTTGTG 1650
25 AGGAGCTGGA AACACATGTT CCCCTTGGGG GTGGTGGATG AACAAAGAGA 1700
AAGAGGGTTT GGAAGCCAGA TCTATGCCAC AAGAACCCCC TTTACCCCCA 1750
TGACCAACAT CGCAGACACA TGTGCTGGCC ACCTGCTGAG CCCCAGTGG 1800
35 AACGAGACAA GCAGCCCTTA GCCCTTCCCC TCTGCAGCTT CCAGGCTGGC 1850
GTGCAGCATC AGCATCCCTA GAAAGCCATG TGCAGCCACC AGTCCATTGG 1900
40 GCAGGCAGAT GTTCCTAATA AAGCTTCTGT TCC 1933

Fig. 2c

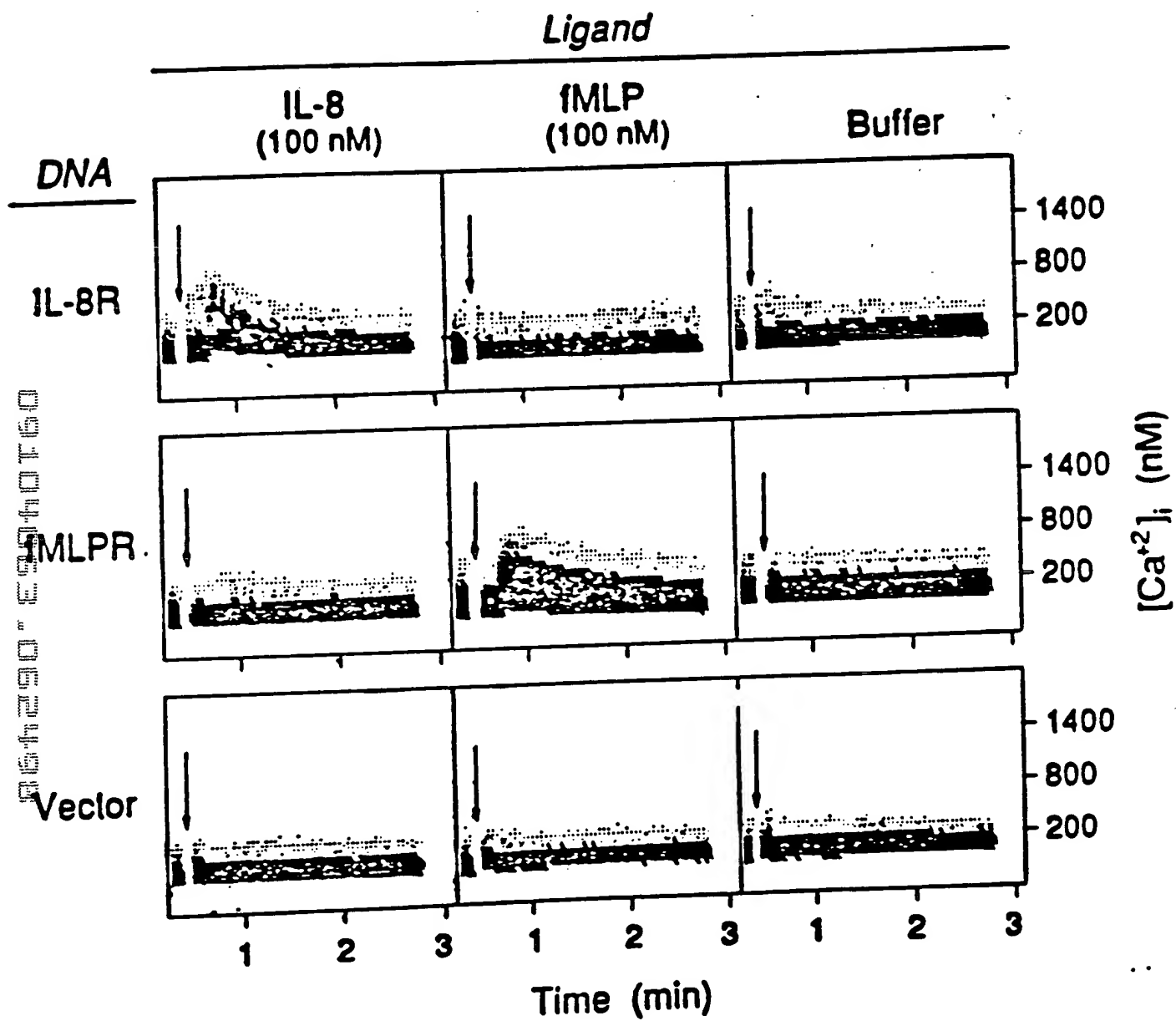


Figure 3a

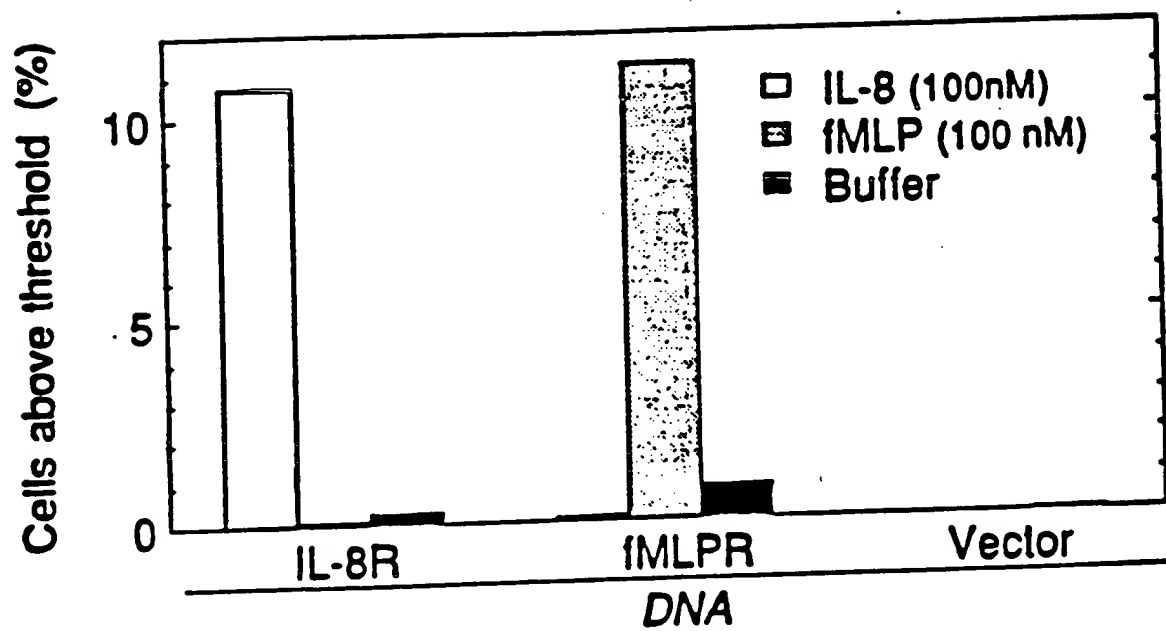


Figure 3b

GAATTCCAGT GTGCTGGCGG CGCGGCGCAA AGTGACGCCG AGGGCCTGAG 50

TGCTCCAGTA GCCACCGCAT CTGGAGAACC AGCGGTTACC ATG GAG 96
Met Glu
1

GGG ATC AGT ATA TAC ACT TCA GAT AAC TAC ACC GAG GAA 135
Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu
5 10 15

ATG GGC TCA GGG GAC TAT GAC TCC ATG AAG GAA CCC TGT 174
Met Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys
20 25

TTC CGT GAA GAA AAT GCT AAT TTC AAT AAA ATC TTC CTG 213
Phe Arg Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu
30 35 40

CCC ACC ATC TAC TCC ATC ATC TTC TTA ACT GGC ATT GTG 252
Pro Thr Ile Tyr Ser Ile Ile Phe Leu Thr Gly Ile Val
45 50

GGC AAT GGA TTG GTC ATC CTG GTC ATG GGT TAC CAG AAG 291
Gly Asn Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys
55 60 65

AAA CTG AGA AGC ATG ACG GAC AAG TAC AGG CTG CAC CTG 330
Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
70 75 80

TCA GTG GCC GAC CTC CTC TTT GTC ATC ACG CTT CCC TTC 369
Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe
85 90

TGG GCA GTT GAT GCC GTG GCA AAC TGG TAC TTT GGG AAC 408
Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn
95 100 105

TTC CTA TGC AAG GCA GTC CAT GTC ATC TAC ACA GTC AAC 447
Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn
110 115

CTC TAC AGC AGT GTC CTC ATC CTG GCC TTC ATC AGT CTG 486
Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu
120 125 130

GAC CGC TAC CTG GCC ATC GTC CAC GCC ACC AAC AGT CAG 525
Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln
135 140 145

AGG CCA AGG AAG CTG TTG GCT GAA AAG GTG GTC TAT GTT 564
Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val
150 155

GGC GTC TGG ATC CCT GCC CTC CTG CTG ACT ATT CCC GAC 603
Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp
160 165 170

Figure 4a

TTC ATC TTT GCC AAC GTC AGT GAG GCA GAT GAC AGA TAT 642
Phe Ile Phe Ala Asn Val Ser Glu Ala Asp Asp Arg Tyr
175 180

ATC TGT GAC CGC TTC TAC CCC AAT GAC TTG TGG GTG GTT 681
Ile Cys Asp Arg Phe Tyr Pr Asn Asp Leu Trp Val Val
185 190 195

GTG TTC CAG TTT CAG CAC ATC ATG GTT GGC CTT ATC CTG 720
Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu
200 205 210

CCT GGT ATT GTC ATC CTG TCC TGC TAT TGC ATT ATC ATC 759
Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile
215 220

TCC AAG CTG TCA CAC TCC AAG GGC CAC CAG AAG CGC AAG 798
Ser Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys
225 230 235

GCC CTC AAG ACC ACA GTC ATC CTC ATC CTG GCT TTC TTC 837
Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
240 245

GCC TGT TGG CTG CCT TAC TAC ATT GGG ATC AGC ATC GAC 876
Ala Cys Trp Leu Pro Tyr Tyr Ile Gly Ile Ser Ile Asp
250 255 260

TCC TTC ATC CTC CTG GAA ATC ATC AAG CAA GGG TGT GAG 915
Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln Gly Cys Glu
265 270 275

TTT GAG AAC ACT GTG CAC AAG TGG ATT TCC ATC ACC GAG 954
Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
280 285

GCC CTA GCT TTC TTC CAC TGT TGT CTG AAC CCC ATC CTC 993
Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu
290 295 300

TAT GCT TTC CTT GGA GCC AAA TTT AAA ACC TCT GCC CAG 1032
Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln
305 310

CAC GCA CTC ACC TCT GTG AGC AGA GGG TCC AGC CTC AAG 1071
His Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys
315 320 325

ATC CTC TCC AAA GGA AAG CGA GGT GGA CAT TCA TCT GTT 1110
Ile Leu Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val
330 335 340

TCC ACT GAG TCT GAG TCT TCA AGT TTT CAC TCC AGC TAAC 1150
Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
345 350 352

ACAGATGTAA AAGACTTTTT TTTATACGAT AAATAACTTT TTTTAAAGTT 1200

Figur 4b

ACACATTTTT CAGATATAAA AGACTGACCA ATATTGTACA GTTTTTATTG 1250
 CTTGTTGGAT TTTTGTCTTG TGTTCCTTA GTTTTTGTA AGTTTAATTG 1300
 ACTTATTAT ATAAATTTTT TTTGTTTCAT ATTGATGTGT GTCTAGGCAG 1350
 GACCTGTGGC CAAGTTCTTA GTTGCTGTAT GTCTCGTGGT AGGACTGTAG 1400
 AAAAGGGAAC TGAACATTCC AGAGCGTGTA GTGAATCAG TAAAGCTAGA 1450
 AATGATCCCC AGCTGTTTAT GCATAGATAA TCTCTCCATT CCCGTGGAAC 1500
 GTTTTTCCTG TTCTTAAGAC GTGATTTTGC TGTAGAAGAT GGCACTTATA 1550
 ACCAAAGCCC AAAGTGGTAT AGAAATGCTG GTTTTTCAGT TTTCAGGAGT 1600
 GGGTTGATTT CAGCACCTAC AGTGTACAGT CTTGTATTAA GTTGTTAATA 1650
 AAAGTACATG TTAACTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1700
 AAAAAAAAAA AAAGCGGCCG CCAGCACACT GGAATTC 1737

09104033.062498

Figure 4c

GAATTCCAGT GTGCTGGCGG CCGCCAGTG TGCTGGCGGC GGCAGTTGAG 50

GGAAAGGACA GAGGTTATGA GTGCCTGCAA GAGTGGCAGC CTGGAGTAGA 100

GAAAACACTA AAGGTGGAGT CAAAAGACCT GAGTTCAAGT CCCAGCTCTG 150

CCACTGGTTA GCTGTGGGAT CTCGGAAAAG ACCCAGTGAA AAAAAAAAAA 200

AAAGTGATGA GTTGTGAGGC AGGTCGCGGC CCTACTGCCT CAGGAGACGA 250

TGCGCAGCTC ATTTGCTTAA ATTTGCAGCT GACGGCTGCC ACCTCTCTAG 300

AGGCACCTGG CGGGGAGCCT CTCAACATAA GACAGTGACC AGTCTGGTGA 350

CTCACAGCCG GCACAGCC ATG AAC TAC CCG CTA ACG CTG GAA 392
Met Asn Tyr Pro Leu Thr Leu Glu
1 5

ATG GAC CTC GAG AAC CTG GAG GAC CTG TTC TGG GAA CTG 431
Met Asp Leu Glu Asn Leu Glu Asp Leu Phe Trp Glu Leu
10 15 20

GAC AGA TTG GAC AAC TAT AAC GAC ACC TCC CTG GTG GAA 470
Asp Arg Leu Asp Asn Tyr Asn Asp Thr Ser Leu Val Glu
25 30

AAT CAT CTC TGC CCT GCC ACA GAG GGG CCC CTC ATG GCC 509
Asn His Leu Cys Pro Ala Thr Glu Gly Pro Leu Met Ala
35 40 45

TCC TTC AAG GCC GTG TTC GTG CCC GTG GCC TAC AGC CTC 548
Ser Phe Lys Ala Val Phe Val Pro Val Ala Tyr Ser Leu
50 55 60

ATC TTC CTC CTG GGC GTG ATC GGC AAC GTC CTG GTG CTG 587
Ile Phe Leu Leu Gly Val Ile Gly Asn Val Leu Val Leu
65 70

GTG ATC CTG GAG CGG CAC CGG CAG ACA CGC AGT TCC ACG 626
Val Ile Leu Glu Arg His Arg Gln Thr Arg Ser Ser Thr
75 80 85

GAG ACC TTC CTG TTC CAC CTG GCC GTG GCC GAC CTC CTG 665
Glu Thr Phe Leu Phe His Leu Ala Val Ala Asp Leu Leu
90 95

CTG GTC TTC ATC TTG CCC TTT GCC GTG GCC GAG GGC TCT 704
Leu Val Phe Ile Leu Pro Phe Ala Val Ala Glu Gly Ser
100 105 110

Figure 5a

GTG	GGC	TGG	GTC	CTG	GGG	ACC	TTC	CTC	TGC	AAA	ACT	GTG	743
Val	Gly	Trp	Val	Leu	Gly	Thr	Phe	Leu	Cys	Lys	Thr	Val	
		115					120					125	
ATT	GCC	CTG	CAC	AAA	GTC	AAC	TTC	TAC	TGC	AGC	AGC	CTG	782
Ile	Ala	Leu	His	Lys	Val	Asn	Phe	Tyr	Cys	Ser	Ser	Leu	
			130					135					
CTC	CTG	GCC	TGC	ATC	GCC	GTG	GAC	CGC	TAC	CTG	GCC	ATT	821
Leu	Leu	Ala	Cys	Ile	Ala	Val	Asp	Arg	Tyr	Leu	Ala	Ile	
	140					145					150		
GTC	CAC	GCC	GTC	CAT	GCC	TAC	CGC	CAC	CGC	CGC	CTC	CTC	860
Val	His	Ala	Val	His	Ala	Tyr	Arg	His	Arg	Arg	Leu	Leu	
			155				160						
TCC	ATC	CAC	ATC	ACC	TGT	GGG	ACC	ATC	TGG	CTG	GTG	GGC	899
Ser	Ile	His	Ile	Thr	Cys	Gly	Thr	Ile	Trp	Leu	Val	Gly	
165					170					175			
TTC	CTC	CTT	GCC	TTG	CCA	GAG	ATT	CTC	TTC	GCC	AAA	GTC	938
Phe	Leu	Leu	Ala	Leu	Pro	Glu	Ile	Leu	Phe	Ala	Lys	Val	
		180					185					190	
AGC	CAA	GGC	CAT	CAC	AAC	AAC	TCC	CTG	CCA	CGT	TGC	ACC	977
Ser	Gln	Gly	His	His	Asn	Asn	Ser	Leu	Pro	Arg	Cys	Thr	
				195				200					
TTC	TCC	CAA	GAG	AAC	CAA	GCA	GAA	ACG	CAT	GCC	TGG	TTC	1016
Phe	Ser	Gln	Glu	Asn	Gln	Ala	Glu	Thr	His	Ala	Trp	Phe	
	205					210					215		
ACC	TCC	CGA	TTC	CTC	TAC	CAT	GTG	GCG	GGA	TTC	CTG	CTG	1055
Thr	Ser	Arg	Phe	Leu	Tyr	His	Val	Ala	Gly	Phe	Leu	Leu	
			220					225					
CCC	ATG	CTG	GTG	ATG	GGC	TGG	TGC	TAC	GTG	GGG	GTA	GTG	1094
Pro	Met	Leu	Val	Met	Gly	Trp	Cys	Tyr	Val	Gly	Val	Val	
230					235					240			
CAC	AGG	TTG	CGC	CAG	GCC	CAG	CGG	CGC	CCT	CAG	CGG	CAG	1133
His	Arg	Leu	Arg	Gln	Ala	Gln	Arg	Arg	Pro	Gln	Arg	Gln	
		245					250					255	
AAG	GCA	GTC	AGG	GTG	GCC	ATC	CTG	GTG	ACA	AGC	ATC	TTC	1172
Lys	Ala	Val	Arg	Val	Ala	Ile	Leu	Val	Thr	Ser	Ile	Phe	
				260					265				
TTC	CTC	TGC	TGG	TCA	CCC	TAC	CAC	ATC	GTC	ATC	TTC	CTG	1211
Phe	Leu	Cys	Trp	Ser	Pro	Tyr	His	Ile	Val	Ile	Phe	Leu	
	270					275					280		
GAC	ACC	CTG	GCG	AGG	CTG	AAG	GCC	GTG	GAC	AAT	ACC	TGC	1250
Asp	Thr	Leu	Ala	Arg	Leu	Lys	Ala	Val	Asp	Asn	Thr	Cys	
			285					290					

Figure 5b

AAG CTG AAT GGC TCT CTC CCC GTG GCC ATC ACC ATG TGT 1289
 Lys Leu Asn Gly Ser Leu Pro Val Ala Ile Thr Met Cys
 295 300 305

GAG TTC CTG GGC CTG GCC CAC TGC TGC CTC AAC CCC ATG 1328
 Glu Phe Leu Gly Leu Ala His Cys Cys Leu Asn Pr Met
 310 315 320

CTC TAC ACT TTC GCC GGC GTG AAG TTC CGC AGT GAC CTG 1367
 Leu Tyr Thr Phe Ala Gly Val Lys Phe Arg Ser Asp Leu
 325 330

TCG CGG CTC CTG ACG AAG CTG GGC TGT ACC GGC CCT GCC 1406
 Ser Arg Leu Leu Thr Lys Leu Gly Cys Thr Gly Pro Ala
 335 340 345

TCC CTG TGC CAG CTC TTC CCT AGC TGG CGC AGG AGC AGT 1445
 Ser Leu Cys Gln Leu Phe Pro Ser Trp Arg Arg Ser Ser
 350 355

CTC TCT GAG TCA GAG AAT GCC ACC TCT CTC ACC ACG TTC TA 1486
 Leu Ser Glu Ser Glu Asn Ala Thr Ser Leu Thr Thr Phe
 360 365 370 372

GGTC CCAAGTGTCCC CTTTTATTGC TGCTTTTCCT TGGGGCAGGC 1530

AGTGATGCTG GATGCTCCTT CCAACAGGAG CTGGGATCCT AAGGGCTCAC 1580

CGTGGCTAAG AGTGTCCTAG GAGTATCCTC ATTTGGGGTA GCTAGAGGAA 1630

CCAACCCCCA TTTCTAGAAC ATCCCGCGGC CGCCAGCACA CTGGAATTC 1679

05104063-062490

Figure 5c

Q¹-COOH



1

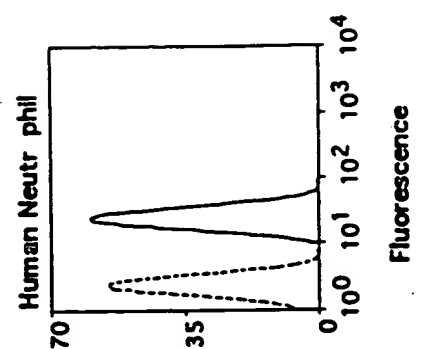
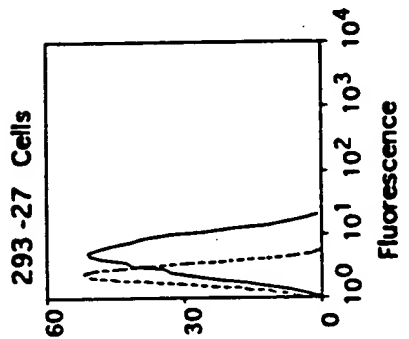
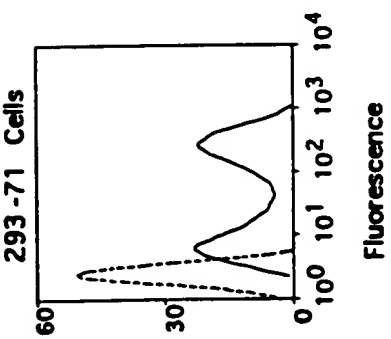
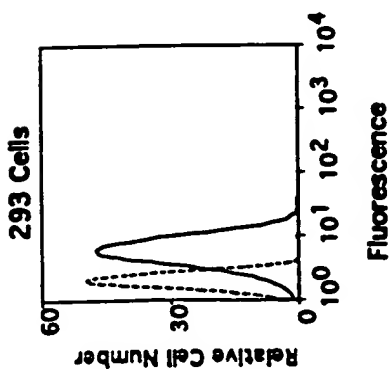


Fig. 1

FIG. 8

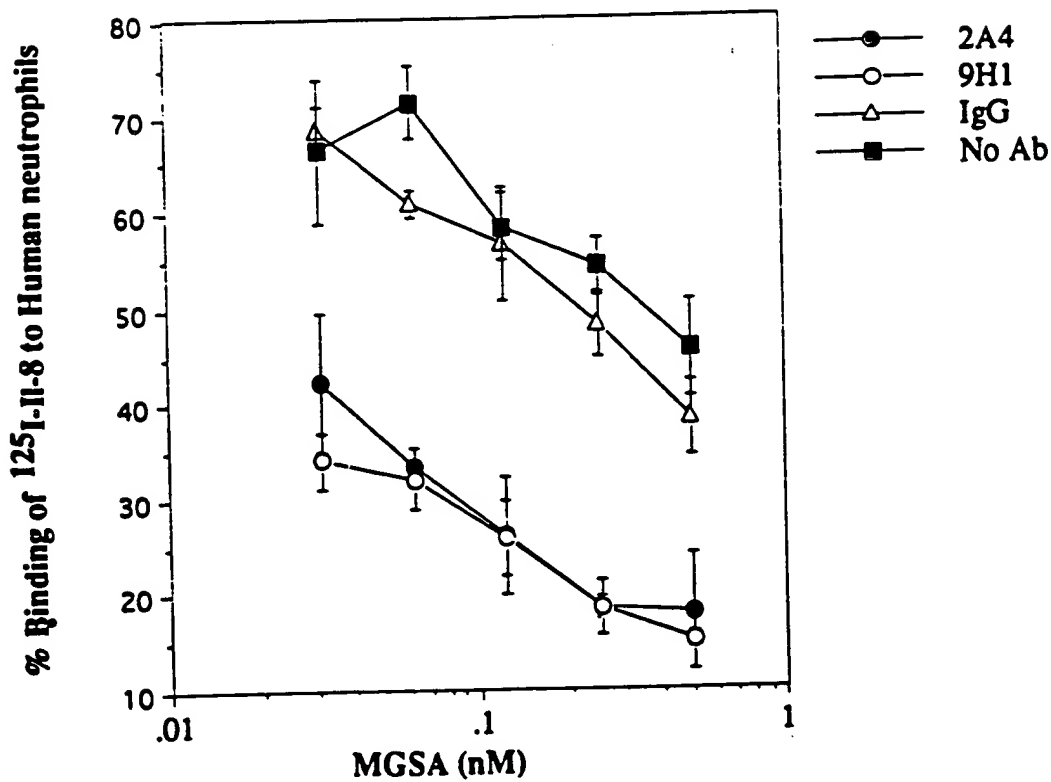
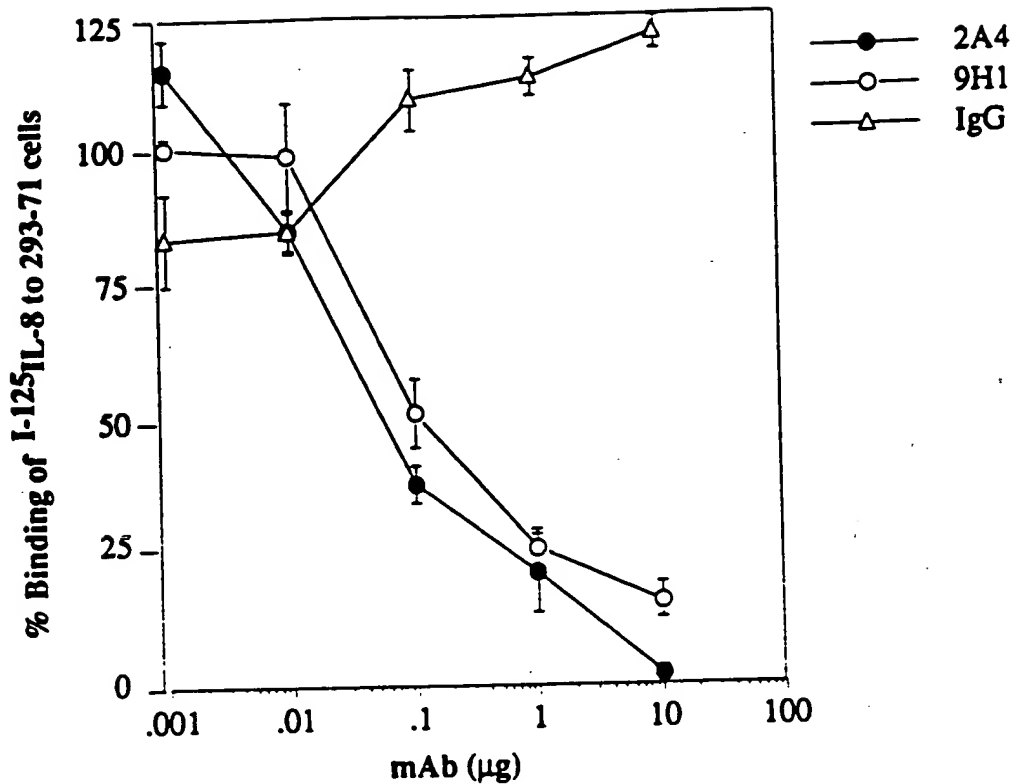
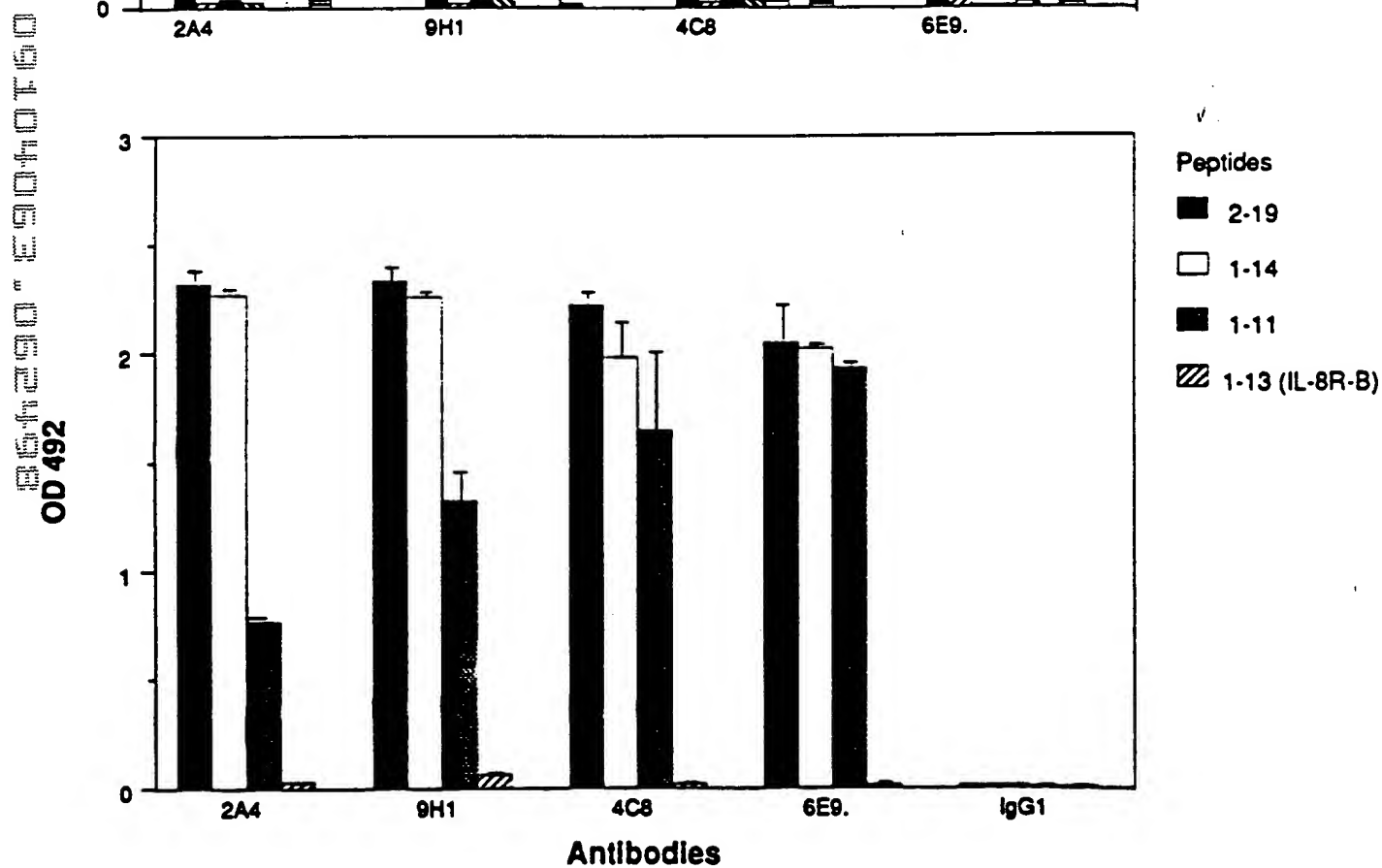
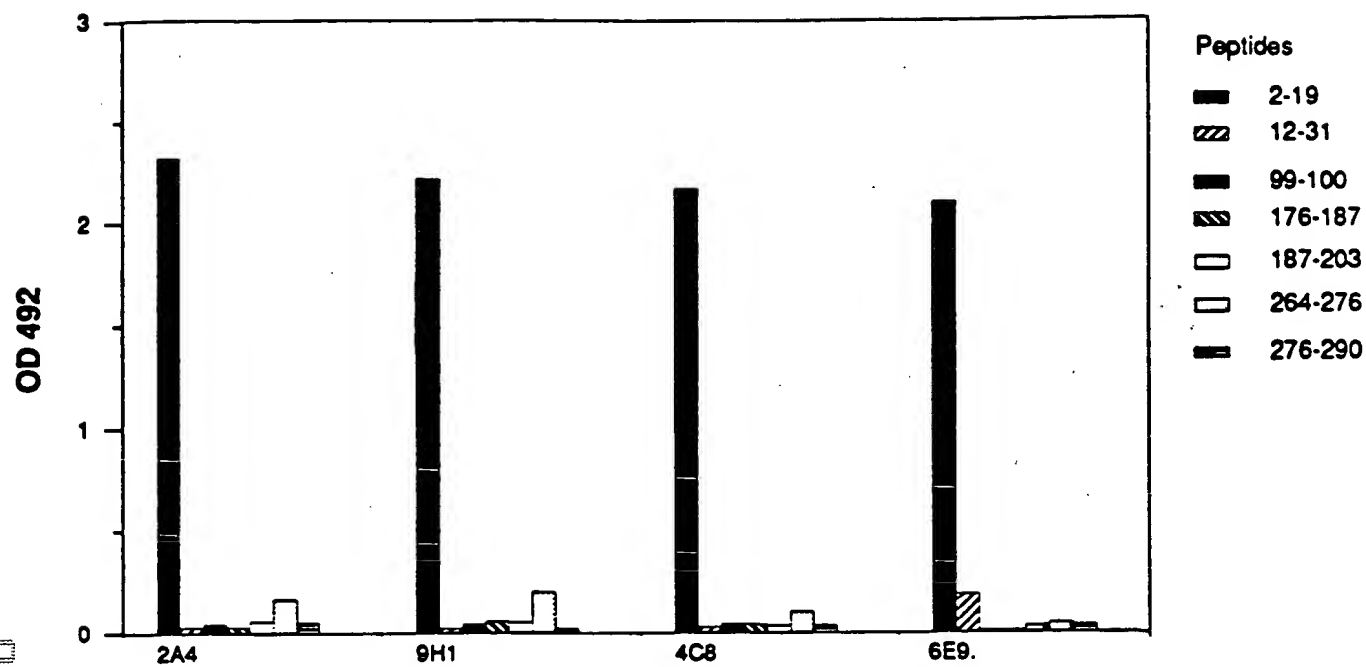


Fig 4



Concentrations of IL8 in Sputum from Patients with Chronic Airway Inflammation and Induced Sputum from Healthy Subjects

